
FACSIMILE MESSAGE - PLEASE DELIVER PROMPTLY

November 11, 2002

TO: Examiner Bridget Bunner
Group 1647
(703) 308-7148

FROM Lin Sun-Hoffman
Celera Genomics Corp.
(240) 453-3628

FAX NO: (703) 308-4242

OF PAGES (incl. cover): 8

Re: U.S. Serial No. 09/776,705, filed Feb. 6, 2001
Entitled "ISOLATED HUMAN TRANSPORTER, NUCLEIC ACID
MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS, AND
USES THEREOF"

A Preliminary Amendment (Restriction Election) and a Statement Regarding Duty of Disclosure and a request of two-month extension of time in the above-identified application follows. No fee is due for this filing.

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: GUEGLER et al.

Art Unit: 1647

Serial No. 09/776,705

Examiner: B. Bunner

Filed: February 6, 2001

Atty. Docket: CL001010

For: ISOLATED HUMAN TRANSPORTER
PROTEINS, NUCLEIC ACID MOLECULES
ENCODING HUMAN TRANSPORTER
PROTEINS, AND USES THEREOF

**Statement Regarding Duty Of Disclose Information Material To Patentability
Under 37 CFR 1.56 (a) and (b)**

Honorable Commissioner of
Patents and Trademarks
Washington, D.C. 20231

By Facsimile

Sir:

This statement is to inform the United States of Patent and Trademark Office that Applicants and their representative have made a good faith effort in searching prior art relating to this invention.

No prior art material to patentability of the present invention has been found. The closest information associated with the invention is disclosed in Figures 1 and 2 in the top BLAST search results. However, this information, by itself or in combination with other information, does not constitute a prima facie case of unpatentability of any of the pending claims. Thus, it does not defeat the novelty of the present invention and the actual underlying references for the top BLAST hits are not being provided.

Respectfully submitted,

CELERA GENOMICS

By: 

Lin Sun-Hoffman, Ph.D., Reg No. 47,983

Date: Nov. 11, 2001

Celera Genomics Corporation
45 West Gude Drive, C2-4#20
Rockville, MD 20850
Tel: 240-453-3628, Fax: 240-453-3084

BLAST SEARCH RESULT AGAINST GENESEQ AND NCBI DATABASE CL001010

BLASTP 2.0.14 [Jun-29-2000]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997). "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs". Nucleic Acids Res. 25:3389-3402.

Query= 1010
(547 letters)

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952,616 sequences; 143,563,330 total letters

Searching.....done

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PPNSKHH
Sbjct: 540 PPNSKHH 546

BLASTP 2.0.14 [Jun-29-2000]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997).
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
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Query= 1010
(547 letters)

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Length = 547

Score = 1084 bits (2774), Expect = 0.0
Identities = 543/547 (99%), Positives = 544/547 (99%)

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Query: 61 KKLADYADEHHPGTTSGMSSFNLNAIMGSGILGLSYAMAYTGVILFIIMLLAVAILSL 120
KKLADYADEHHPGTTSGMSSFNLNAIMGSGILGLSYAMA TG+ILFIIMLLAVAILSL
Sbjct: 61 KKLADYADEHHPGTTSGMSSFNLNAIMGSGILGLSYAMANTGILFIIMLLAVAILSL 120

Query: 121 YSVHLLKTAKEGGSLIYEKLGKAFGWPGKIGAFVSITMQNIGAMSSYLFIIKYELPEV 180
YSVHLLKTAKEGGSLIYEKLGKAFGWPGKIGAFVSITMQNIGAMSSYLFIIKYELPEV
Sbjct: 121 YSVHLLKTAKEGGSLIYEKLGKAFGWPGKIGAFVSITMQNIGAMSSYLFIIKYELPEV 180

Query: 181 IRAFMGLEENTGEWYLNNGNYLIHFVSVGIHLPLSLLKNLGYLGYSFGSLTCMVFFVSVV 240
IRAFMGLEENTGEWYLNNGNYLIHFVSVGIHLPLSLLKNLGYLGYSFGSLTCMVFFVSVV
Sbjct: 181 IRAFMGLEENTGEWYLNNGNYLIHFVSVGIHLPLSLLKNLGYLGYSFGSLTCMVFFVSVV 240

Query: 241 IYKKFQIPCLPLVDHSGVGNLSFNNTLPMHVVMPLPNSESDVNFMMMDYTHRNPAGLDEN 300
IYKKFQIPCLPLVDHSGVGNLSFNNTLPMHVVMPLPNSESDVNFMMMDYTHRNPAGLDEN
Sbjct: 241 IYKKFQIPCLPLVDHSGVGNLSFNNTLPMHVVMPLPNSESDVNFMMMDYTHRNPAGLDEN 300

Query: 301 QAKGSLHDSGVEYEAHSDDKCEPKYFVFNSTAYAIPILVFAFVCHPEVLPIYSELKDRS 360
QAKGSLHDSGVEYEAHSDDKCEPKYFVFNSTAYAIPILVFAFVCHPEVLPIYSELKDRS
Sbjct: 301 QAKGSLHDSGVEYEAHSDDKCEPKYFVFNSTAYAIPILVFAFVCHPEVLPIYSELKDRS 360

Query: 361 RRKMQTVSNISITGMLVMYLLAALFGYLTIFYGEVEDELLHAYSKVYTLDIPLLMVRLAVL 420
RRKMQTVSNISITGMLVMYLLAALFGYLTIFYGEVEDELLHAYSKVYTLDIPLLMVRLAVL
Sbjct: 361 RRKMQTVSNISITGMLVMYLLAALFGYLTIFYGEVEDELLHAYSKVYTLDIPLLMVRLAVL 420

Query: 421 VAVTQTVPIVLPFIRTSVITLLFPKRPFSWIRHFLIAAVLIALNNVLVILVPTIKYIFGF 480
VAVT TVPIVLPFIRTSVITLLFPKRPFSWIRHFLIAAVLIALNNVLVILVPTIKYIFGF
Sbjct: 421 VAVTLTVPIVLPFIRTSVITLLFPKRPFSWIRHFLIAAVLIALNNVLVILVPTIKYIFGF 480

Query: 481 IGASSATMLIFILPAVFYKLKLVKKETFRSPQKVGALIFLVVGIFFMIGSMALIHDWIYD 540
IGASSATMLIFILPAVFYKLKLVKKETFRSPQKVGALIFLVVGIFFMIGSMALIHDWIYD
Sbjct: 481 IGASSATMLIFILPAVFYKLKLVKKETFRSPQKVGALIFLVVGIFFMIGSMALIHDWIYD 540

Query: 541 PPNSKHH 547
PPNSKHH
Sbjct: 541 PPNSKHH 547

>CRA|225000041339589 /altid=gi|19169919 /def=emb|CAD26771.1| unnamed
protein product [Homo sapiens] /org=Homo sapiens
/taxon=9606 /div=PRI /dataset=pataa /length=487
Length = 487

Score = 476 bits (1212), Expect = e-134
Identities = 258/543 (47%), Positives = 350/543 (63%), Gaps = 67/543 (12%)

Query 5 ELRNVNIEPDDESSGESAPDSYIRIGNSEKAAMSSQFANEDTESQKFLTNGFLGKKKLA 64
EL+N++P+D++S+S++N++S+F+DES++LTN L KKK
Sbjct: 12 ELQNMVTV-PEDDNISNDS--NDFTEVENGQ---INSKFIS-DRESRRSLTNSHLEKKK-- 62

Query: 65 DYADEHHPGTTSGMSSFNLNAIMGSGILGLSYAMAYTGVILFIIMLLAVAILSLYSVH 124
DE+HPGTTSGMSSFNLNAI+GSGILGLSYAMA TG+LF+++L+V+LS+YS++
Sbjct: 63 --CDEYHPGTTSGMSSVFNLSNAIVGSGILGLSYAMANTGIALFMVLLTSVTLLSIYSIN 120

Query: 125 LLLKTAKEGGSLIYEKLGKAFGWPGKIGAFVSITMQNIGAMSSYLFIIKYELPEVIRAF 184
LLL +KE G++YEKLG+ FG GK F++QN GAM SYLFI+K ELP I+

Shjct: 121 LLLICSKETGCMVYEKLGEQVFGTTGKFVIFGATSLQNTGAMLSYLFIVKNELP SAIKFL 180

Query: 185 MGLEENTGEWYLNNGNYLIHFVSVGILPLSLLKNLGYLGYTSGFSLTCMVFFVS VVIYKK 244
MG EE WY++G L++ V+ GILPL LLKNLGYLGYTSGFSL+CMVFF+ VVIYKK

Shjct: 181 MGKEETFSAWYVDGRVLVVIVTFGILPLCLLKNLGYLGYTSGFSLSCMVFFLIVVIYKK 240

Query: 245 FQIPCPLPVLDSVGNLSFNNTLPMHVVMPLPNSESSDVNFMMDYTHRNPAGLDENQAKG 304
FQIPC +P L+ ++ NS ++D

Shjct: 241 FQIPCIVPELNSTIS-----ANSTNADT----- 263

Query: 305 SLHDSGVEYEAHSDDKCEPKYFVFNSTAYAIPILVFAFVCHPEVLPIYSELKDRSRRKM 364
C PKY FNS+T YA+P + FAFVCHP VLPIYSELKDRS++KM

Shjct: 264 -----CTPKYVTFNSTKYALPTIAFAFVCHPSVLPIYSELKDRSQKKM 307

Query: 365 QTVSNISITGMLVMYLLAALFGYLTFYGEVEDELLHAYSKVYTLDIPLLMVRLAVLVAVT 424
Q VSNIS M VMY L A+FGYLTFY V+ +LLH Y DI+L VRLAV+VAV

Shjct: 308 QMVSNISFFAMFVMYFLTAIFGYLTFYDNVQSDLLHKYQS--KDDILILTVRLAVIVAVI 365

Query: 425 QTVPIVLFPIRTSVITLLFPKRPFWSIRHFLIAAVLIALNNVLVILVPTIKYIFGFIGAS 484
TVP++ F +R+S+ L K F+ RH ++ +L+ + N+LVI +P++K IFG +G +

Shjct: 366 LTVPVLFFTVRSSLFELA-KKTKFNLCRHTVVTCLLVVINLLVIFIPSMKDIFGVVGVT 424

Query: 485 SATMLIFILPAVFYLLKLVKKETFRSPQKVGALIFLVVGIFFMIGSMALIIDWIYDPPNS 544
SA MLIFILP+ YLK+ ++ + Q++ A +FL +G+ F+ S+ L+IDW +

Shjct: 425 SANMLIFILPSSLYLKITDQDGDGKTQRIWAALFLGLGVLFSLVSIPLVIYDWACSSSSD 484

Query: 545 KHH 547
+ H

Shjct: 485 EGH 487